

0590  
12/10

OIEP

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/991,225

DATE: 12/03/2001  
TIME: 14:25:07

Input Set : A:\es.txt  
Output Set: N:\CRF3\11212001\I991225.raw

**ENTERED**

3 <110> APPLICANT: Bristol-Myers Squibb Company  
5 <120> TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY11,  
EXPRESSED HIGHLY IN

6 HEART AND VARIANTS THEREOF

8 <130> FILE REFERENCE: D0075.NP

C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/991,225

C--> 10 <141> CURRENT FILING DATE: 2001-11-16

10 <150> PRIOR APPLICATION NUMBER: 60/249,613

11 <151> PRIOR FILING DATE: 2000-11-17

13 <150> PRIOR APPLICATION NUMBER: 60/257,611

14 <151> PRIOR FILING DATE: 2000-12-21

16 <150> PRIOR APPLICATION NUMBER: 60/305,818

17 <151> PRIOR FILING DATE: 2001-07-16

19 <160> NUMBER OF SEQ ID NOS: 81

21 <170> SOFTWARE: PatentIn version 3.0

23 <210> SEQ ID NO: 1

24 <211> LENGTH: 1708

25 <212> TYPE: DNA

26 <213> ORGANISM: homo sapiens

28 <220> FEATURE:

29 <221> NAME/KEY: CDS

30 <222> LOCATION: (515)..(1504)

32 <400> SEQUENCE: 1

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33 cccacgcgtc cggggagctt gcactaacat ctacaatggc ttctaaaaag cacagatgac      60
35 ctgctacact tcttgacttg cttgctattg gttggcactg ttcataaata taatttgctc      120
37 ttctactttt ctttgaaatg agcaacctga attactcgga ggagaaaggc aggagagata      180
39 gaggcagcag aagccagggc agctgaaaga cagagacctt cagtctgaac caacaacaag      240
41 caaagttaaa ttatggatat ccaagggagt ctatagaagg tccatgcaag acattttgac      300
43 tacttgtctg aactagatat cccttgaatg tgcacacaaa aagtgaatgg gtcatttgat      360
45 aagggaacac taggttccaa gatggctgaa taggaagagc tccagtctgc agatcccagt      420
47 gtgagcaacg tggaagatgg gtgatttctg catttccaac tgagcatgga gagaaaaatt      480
49 tatgtccttg caaccatcca tctcogtata agaa atg gaa cca aat ggc acc ttc      535
50                                     Met Glu Pro Asn Gly Thr Phe
51                                     1               5
53 agc aat aac aac agc agg aac tgc aca att gaa aac ttc aag aga gaa      583
54 Ser Asn Asn Asn Ser Arg Asn Cys Thr Ile Glu Asn Phe Lys Arg Glu
55      10               15               20
57 ttt ttc cca att gta tat ctg ata ata ttt ttc tgg gga gtc ttg gga      631
58 Phe Phe Pro Ile Val Tyr Leu Ile Ile Phe Phe Trp Gly Val Leu Gly
59      25               30               35
61 aat ggg ttg tcc ata tat gtt ttc ctg cag cct tat aag aag tcc aca      679
62 Asn Gly Leu Ser Ile Tyr Val Phe Leu Gln Pro Tyr Lys Lys Ser Thr
63 40               45               50               55
65 tct gtg aac gtt ttc atg cta aat ctg gcc att tca gat ctc ctg ttc      727
66 Ser Val Asn Val Phe Met Leu Asn Leu Ala Ile Ser Asp Leu Leu Phe
67      60               65               70
69 ata agc acg ctt ccc ttc agg gct gac tat tat ctt aga ggc tcc aat      775
70 Ile Ser Thr Leu Pro Phe Arg Ala Asp Tyr Tyr Leu Arg Gly Ser Asn

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|     |   |   |     |   |
|-----|---|---|-----|---|
| 71  | 75  | 80  | 85  |   |
| 73  | tggaata   | tttgga  | gac | ctg gcc tgc agg att atg tct tat tcc ttg tat 823 |
| 74  | Trp Ile Phe   | Gly Asp Leu Ala Cys Arg Ile Met Ser Tyr Ser Leu Tyr |     |   |
| 75  | 90  | 95  | 100 |   |
| 77  | gtc aac atg tac agc agt att tat ttc ctg acc gtg ctg agt gtt gtg |   |     | 871   |
| 78  | Val Asn Met Tyr Ser Ser Ile Tyr Phe Leu Thr Val Leu Ser Val Val |   |     |   |
| 79  | 105   | 110   | 115 |   |
| 81  | cgt ttc ctg gca atg gtt cac ccc ttt cgg ctt ctg cat gtc acc agc |   |     | 919   |
| 82  | Arg Phe Leu Ala Met Val His Pro Phe Arg Leu Leu His Val Thr Ser |   |     |   |
| 83  | 120   | 125   | 130 | 135   |
| 85  | atc agg agt gcc tgg atc ctc tgt ggg atc ata tgg atc ctt atc atg |   |     | 967   |
| 86  | Ile Arg Ser Ala Trp Ile Leu Cys Gly Ile Ile Trp Ile Leu Ile Met |   |     |   |
| 87  | 140   | 145   | 150 |   |
| 89  | gct tcc tca ata atg ctc ctg gac agt ggc tct gag cag aac ggc agt |   |     | 1015  |
| 90  | Ala Ser Ser Ile Met Leu Leu Asp Ser Gly Ser Glu Gln Asn Gly Ser |   |     |   |
| 91  | 155   | 160   | 165 |   |
| 93  | gtc aca tca tgc tta gag ctg aat ctc tat aaa att gct aag ctg cag |   |     | 1063  |
| 94  | Val Thr Ser Cys Leu Glu Leu Asn Leu Tyr Lys Ile Ala Lys Leu Gln |   |     |   |
| 95  | 170   | 175   | 180 |   |
| 97  | acc atg aac tat att gcc ttg gtg gtg ggc tgc ctg ctg cca ttt ttc |   |     | 1111  |
| 98  | Thr Met Asn Tyr Ile Ala Leu Val Val Gly Cys Leu Leu Pro Phe Phe |   |     |   |
| 99  | 185   | 190   | 195 |   |
| 101 | aca ctc agc atc tgt tat ctg ctg atc att cgg gtt ctg tta aaa gtg |   |     | 1159  |
| 102 | Thr Leu Ser Ile Cys Tyr Leu Leu Ile Ile Arg Val Leu Leu Lys Val |   |     |   |
| 103 | 200   | 205   | 210 | 215   |
| 105 | gag gtc cca gaa tcg ggg ctg cgg gtt tct cac agg aag gca ctg acc |   |     | 1207  |
| 106 | Glu Val Pro Glu Ser Gly Leu Arg Val Ser His Arg Lys Ala Leu Thr |   |     |   |
| 107 | 220   | 225   | 230 |   |
| 109 | acc atc atc atc acc ttg atc atc ttc ttc ttg tgt ttc ctg ccc tat |   |     | 1255  |
| 110 | Thr Ile Ile Ile Thr Leu Ile Ile Phe Phe Leu Cys Phe Leu Pro Tyr |   |     |   |
| 111 | 235   | 240   | 245 |   |
| 113 | cac aca ctg agg acc gtc cac ttg acg aca tgg aaa gtg ggt tta tgc |   |     | 1303  |
| 114 | His Thr Leu Arg Thr Val His Leu Thr Thr Trp Lys Val Gly Leu Cys |   |     |   |
| 115 | 250   | 255   | 260 |   |
| 117 | aaa gac aga ctg cat aaa gct ttg gtt atc aca ctg gcc ttg gca gca |   |     | 1351  |
| 118 | Lys Asp Arg Leu His Lys Ala Leu Val Ile Thr Leu Ala Leu Ala Ala |   |     |   |
| 119 | 265   | 270   | 275 |   |
| 121 | gcc aat gcc tgc ttc aat cct ctg ctc tat tac ttt gct ggg gag aat |   |     | 1399  |
| 122 | Ala Asn Ala Cys Phe Asn Pro Leu Leu Tyr Tyr Phe Ala Gly Glu Asn |   |     |   |
| 123 | 280   | 285   | 290 | 295   |
| 125 | ttt aag gac aga cta aag tct gca ctc aga aaa ggc cat cca cag aag |   |     | 1447  |
| 126 | Phe Lys Asp Arg Leu Lys Ser Ala Leu Arg Lys Gly His Pro Gln Lys |   |     |   |
| 127 | 300   | 305   | 310 |   |
| 129 | gca aag aca aag tgt gtt ttc cct gtt agt gtg tgg ttg aga aag gaa |   |     | 1495  |
| 130 | Ala Lys Thr Lys Cys Val Phe Pro Val Ser Val Trp Leu Arg Lys Glu |   |     |   |
| 131 | 315   | 320   | 325 |   |
| 133 | aca aga gta taaggagctc ttagatgaga cctgttcttg tatecttg           |   |     | 1544  |
| 134 | Thr Arg Val   |   |     |   |
| 135 | 330   |   |     |   |

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137 tccatcttca ttcaactcata gtctccaaat gactttgtat ttacatcact cccaacaaat 1604
139 gttgattctt aatatttagt tgaccattac ttttgtaaat aagacctact tcaaaaattt 1664
141 tattcagtgt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1708
144 <210> SEQ ID NO: 2
145 <211> LENGTH: 330
146 <212> TYPE: PRT
147 <213> ORGANISM: homo sapiens
149 <400> SEQUENCE: 2
151 Met Glu Pro Asn Gly Thr Phe Ser Asn Asn Asn Ser Arg Asn Cys Thr
152 1 5 10 15
155 Ile Glu Asn Phe Lys Arg Glu Phe Phe Pro Ile Val Tyr Leu Ile Ile
156 20 25 30
159 Phe Phe Trp Gly Val Leu Gly Asn Gly Leu Ser Ile Tyr Val Phe Leu
160 35 40 45
163 Gln Pro Tyr Lys Lys Ser Thr Ser Val Asn Val Phe Met Leu Asn Leu
164 50 55 60
167 Ala Ile Ser Asp Leu Leu Phe Ile Ser Thr Leu Pro Phe Arg Ala Asp
168 65 70 75 80
171 Tyr Tyr Leu Arg Gly Ser Asn Trp Ile Phe Gly Asp Leu Ala Cys Arg
172 85 90 95
175 Ile Met Ser Tyr Ser Leu Tyr Val Asn Met Tyr Ser Ser Ile Tyr Phe
176 100 105 110
179 Leu Thr Val Leu Ser Val Val Arg Phe Leu Ala Met Val His Pro Phe
180 115 120 125
183 Arg Leu Leu His Val Thr Ser Ile Arg Ser Ala Trp Ile Leu Cys Gly
184 130 135 140
187 Ile Ile Trp Ile Leu Ile Met Ala Ser Ser Ile Met Leu Leu Asp Ser
188 145 150 155 160
191 Gly Ser Glu Gln Asn Gly Ser Val Thr Ser Cys Leu Glu Leu Asn Leu
192 165 170 175
195 Tyr Lys Ile Ala Lys Leu Gln Thr Met Asn Tyr Ile Ala Leu Val Val
196 180 185 190
199 Gly Cys Leu Leu Pro Phe Phe Thr Leu Ser Ile Cys Tyr Leu Leu Ile
200 195 200 205
203 Ile Arg Val Leu Leu Lys Val Glu Val Pro Glu Ser Gly Leu Arg Val
204 210 215 220
207 Ser His Arg Lys Ala Leu Thr Thr Ile Ile Ile Thr Leu Ile Ile Phe
208 225 230 235 240
211 Phe Leu Cys Phe Leu Pro Tyr His Thr Leu Arg Thr Val His Leu Thr
212 245 250 255
215 Thr Trp Lys Val Gly Leu Cys Lys Asp Arg Leu His Lys Ala Leu Val
216 260 265 270
219 Ile Thr Leu Ala Leu Ala Ala Asn Ala Cys Phe Asn Pro Leu Leu
220 275 280 285
223 Tyr Tyr Phe Ala Gly Glu Asn Phe Lys Asp Arg Leu Lys Ser Ala Leu
224 290 295 300
227 Arg Lys Gly His Pro Gln Lys Ala Lys Thr Lys Cys Val Phe Pro Val
228 305 310 315 320
231 Ser Val Trp Leu Arg Lys Glu Thr Arg Val

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Input Set : A:\es.txt

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232                               325                               330
235 <210> SEQ ID NO: 3
236 <211> LENGTH: 362
237 <212> TYPE: PRT
238 <213> ORGANISM: homo sapiens.
240 <400> SEQUENCE: 3
242 Met Thr Glu Ala Leu Ile Ser Ala Ala Leu Asn Gly Thr Gln Pro Glu
243 1                               5                               10                               15
245 Leu Leu Ala Gly Gly Trp Ala Ala Gly Asn Ala Thr Thr Lys Cys Ser
246                               20                               25                               30
248 Leu Thr Lys Thr Gly Phe Gln Phe Tyr Tyr Leu Pro Thr Val Tyr Ile
249                               35                               40                               45
251 Leu Val Phe Ile Thr Gly Phe Leu Gly Asn Ser Val Ala Ile Trp Met
252                               50                               55                               60
254 Phe Val Phe His Met Arg Pro Trp Ser Gly Ile Ser Val Tyr Met Phe
255 65                               70                               75                               80
257 Asn Leu Ala Leu Ala Asp Phe Leu Tyr Val Leu Thr Leu Pro Ala Leu
258                               85                               90                               95
260 Ile Phe Tyr Tyr Phe Asn Lys Thr Asp Trp Ile Phe Gly Asp Val Met
261                               100                              105                              110
263 Cys Lys Leu Gln Arg Phe Ile Phe His Val Asn Leu Tyr Gly Ser Ile
264                               115                              120                              125
266 Leu Phe Leu Thr Cys Ile Ser Val His Arg Tyr Thr Gly Val Val His
267                               130                              135                              140
269 Pro Leu Lys Ser Leu Gly Arg Leu Lys Lys Lys Asn Ala Val Tyr Val
270 145                              150                              155                              160
272 Ser Ser Leu Val Trp Ala Leu Val Val Ala Val Ile Ala Pro Ile Leu
273                               165                              170                              175
275 Phe Tyr Ser Gly Thr Gly Val Arg Arg Asn Lys Thr Ile Thr Cys Tyr
276                               180                              185                              190
278 Asp Thr Thr Ala Asp Glu Tyr Leu Arg Ser Tyr Phe Val Tyr Ser Met
279                               195                              200                              205
281 Cys Thr Thr Val Phe Met Phe Cys Ile Pro Phe Ile Val Ile Leu Gly
282                               210                              215                              220
284 Cys Tyr Gly Leu Ile Val Lys Ala Leu Ile Tyr Lys Asp Leu Asp Asn
285 225                              230                              235                              240
287 Ser Pro Leu Arg Arg Lys Ser Ile Tyr Leu Val Ile Ile Val Leu Thr
288                               245                              250                              255
290 Val Phe Ala Val Ser Tyr Leu Pro Phe His Val Met Lys Thr Leu Asn
291                               260                              265                              270
293 Leu Arg Ala Arg Leu Asp Phe Gln Thr Pro Gln Met Cys Ala Phe Asn
294                               275                              280                              285
296 Asp Lys Val Tyr Ala Thr Tyr Gln Val Thr Arg Gly Leu Ala Ser Leu
297                               290                              295                              300
299 Asn Ser Ser Cys Val Asp Pro Ile Leu Tyr Phe Leu Ala Gly Asp Thr Phe
300 305                              310                              315                              320
302 Arg Arg Arg Leu Ser Arg Ala Thr Arg Lys Ser Ser Arg Arg Ser Glu
303                               325                              330                              335
305 Pro Asn Val Gln Ser Lys Ser Glu Glu Met Thr Leu Asn Ile Leu Thr

```

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Output Set: N:\CRF3\11212001\I991225.raw

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306          340          345          350
308 Glu Tyr Lys Gln Asn Gly Asp Thr Ser Leu
309          355          360
311 <210> SEQ ID NO: 4
312 <211> LENGTH: 362
313 <212> TYPE: PRT
314 <213> ORGANISM: homo sapiens
316 <400> SEQUENCE: 4
318 Met Thr Glu Ala Leu Ile Ser Ala Ala Leu Asn Gly Thr Gln Pro Glu
319 1          5          10          15
321 Leu Leu Ala Gly Gly Trp Ala Ala Gly Asn Ala Ser Thr Lys Cys Ser
322          20          25          30
324 Leu Thr Lys Thr Gly Phe Gln Phe Tyr Tyr Leu Pro Thr Val Tyr Ile
325          35          40          45
327 Leu Val Phe Ile Thr Gly Phe Leu Gly Asn Ser Val Ala Ile Trp Met
328          50          55          60
330 Phe Val Phe His Met Arg Pro Trp Ser Gly Ile Ser Val Tyr Met Phe
331 65          70          75          80
333 Asn Leu Ala Leu Ala Asp Phe Leu Tyr Val Leu Thr Leu Pro Ala Leu
334          85          90          95
336 Ile Phe Tyr Tyr Phe Asn Lys Thr Asp Trp Ile Phe Gly Asp Val Met
337          100         105         110
339 Cys Lys Leu Gln Arg Phe Ile Phe His Val Asn Leu Tyr Gly Ser Ile
340          115         120         125
342 Leu Phe Leu Thr Cys Ile Ser Val His Arg Tyr Thr Gly Val Val His
343          130         135         140
345 Pro Leu Lys Ser Leu Gly Arg Leu Lys Lys Lys Asn Ala Val Tyr Val
346 145         150         155         160
348 Ser Ser Leu Val Trp Ala Leu Val Val Ala Val Ile Ala Pro Ile Leu
349          165         170         175
351 Phe Tyr Ser Gly Thr Gly Val Arg Arg Asn Lys Thr Ile Thr Cys Tyr
352          180         185         190
354 Asp Thr Thr Ala Asp Glu Tyr Leu Arg Ser Tyr Phe Val Tyr Ser Met
355          195         200         205
357 Cys Thr Thr Val Phe Met Phe Cys Ile Pro Phe Ile Val Ile Leu Gly
358          210         215         220
360 Cys Tyr Gly Leu Ile Val Lys Ala Leu Ile Tyr Lys Asp Leu Asp Asn
361 225         230         235         240
363 Ser Pro Leu Arg Arg Lys Ser Ile Tyr Leu Val Ile Ile Val Leu Thr
364          245         250         255
366 Val Phe Ala Val Ser Tyr Leu Pro Phe His Val Met Lys Thr Leu Asn
367          260         265         270
369 Leu Arg Ala Arg Leu Asp Phe Gln Thr Pro Gln Met Cys Ala Phe Asn
370          275         280         285
372 Asp Lys Val Tyr Ala Thr Tyr Gln Val Thr Arg Gly Leu Ala Ser Leu
373          290         295         300
375 Asn Ser Cys Val Asp Pro Ile Leu Tyr Phe Leu Ala Gly Asp Thr Phe
376 305         310         315         320
378 Arg Arg Arg Leu Ser Arg Ala Thr Arg Lys Ser Ser Arg Arg Ser Glu

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 Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

## VERIFICATION SUMMARY

DATE: 12/03/2001

PATENT APPLICATION: US/09/991,225

TIME: 14:25:08

Input Set : A:\es.txt

Output Set: N:\CRF3\11212001\I991225.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No  
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:1794 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:80  
L:1812 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:80  
L:1814 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:80  
L:1820 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:81  
L:1838 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:81  
L:1840 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:81